==========
Sequence Listing was accepted.
See attached Validation Report.
If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).
Reviewer: Keisha Douglas
Timestamp: [year=2007; month=11; day=29; hr=17; min=3; sec=36; ms=758;]
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Validated By CRFValidator v 1.0.3

Application No: 10534571 Version No: 1.1

Input Set:

Output Set:

Started: 2007-11-29 17:02:45.660
Finished: 2007-11-29 17:02:47.073
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 413 ms
Total Warnings: 26
Total Errors: 0
No. of SeqIDs Defined: 27
Actual SeqID Count: 27

Error code		Error Description
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W	213	Artificial or Unknown found in <213> in SEQ ID (2)
W	213	Artificial or Unknown found in <213> in SEQ ID (3)
W	213	Artificial or Unknown found in <213> in SEQ ID (4)
W	213	Artificial or Unknown found in <213> in SEQ ID (5)
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W	213	Artificial or Unknown found in <213> in SEQ ID (7)
W	213	Artificial or Unknown found in <213> in SEQ ID (8)
W	213	Artificial or Unknown found in <213> in SEQ ID (9)
W	213	Artificial or Unknown found in <213> in SEQ ID (10)
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W	213	Artificial or Unknown found in <213> in SEQ ID (18)
W	213	Artificial or Unknown found in <213> in SEQ ID (19)
W	213	Artificial or Unknown found in <213> in SEQ ID (20)

Input Set:

Output Set:

Started: 2007-11-29 17:02:45.660
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Total Warnings: 26
Total Errors: 0
No. of SeqIDs Defined: 27
Actual SeqID Count: 27

Error code	Error Description

This error has occured more than 20 times, will not be displayed

SEQUENCE LISTING

<110> WASHINGTON UNIVERSITY

<120> HIGHLY PERMISSIVE CELL LINES FOR HEPATITIS C VIRUS
RNA REPLICATION

<130> 56029-54474

<140> 10/534,571
<141> 2005-10-11

<150> PCT/US03/036634
<151> 2003-11-13

<150> 60/426,256
<151> 2002-11-13

<160> 27

<170> PatentIn Ver. 3.3

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primer

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<210> 2
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<212> DNA
<213> Artificial Sequence

<220>
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primer

<400> 2
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<210> 3
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
probe

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<210> 4
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligodeoxynucleotide

<400> 4
ccctctagaa cgccccgaaa cctagggtgg cg 32

<210> 5
<211> 29
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
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<400> 5
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<210> 6
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<212> DNA
<213> Artificial Sequence

<220>
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ccagctgtct gcgccttcc 79

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<220>
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<210> 8
<211> 49
<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
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<212> DNA
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<220>
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oligodeoxynucleotide

<400> 9
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<212> DNA
<213> Artificial Sequence

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oligodeoxynucleotide

<400> 10
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<210> 11
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
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<400> 11
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<210> 12
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
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oligodeoxynucleotide

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<210> 13
<211> 21
<212> DNA
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<220>
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<210> 14
<211> 92
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligodeoxynucleotide

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ttcgtgctca ttattatcgt gtttttcaaa gg 92

<210> 15
<211> 80
<212> DNA
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<220>
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<212> DNA
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cccagctgtc tgcgccttcc 80

<210> 17
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<212> DNA
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accagctgtc tgcgccttcc 80

<210> 18
<211> 80
<212> DNA
<213> Artificial Sequence

<220>
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oligodeoxynucleotide

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aacagctgtc tgcgccttcc 80

<210> 19
<211> 80
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligodeoxynucleotide

<400> 19
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cacagctgtc tgcgccttcc 80

<210> 20
<211> 80
<212> DNA
<213> Artificial Sequence

<220>
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oligodeoxynucleotide

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tccagctgtc tgcgccttcc 80

<210> 21
<211> 80
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligodeoxynucleotide

<400> 21
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tccagctgtc tgcgccttcc 80

<210> 22
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<212> DNA
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oligodeoxynucleotide

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agggtcgata c 71

<210> 23
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<212> DNA
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<400> 23
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tcc 63

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<212> DNA
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oligodeoxynucleotide

<400> 24

ccgcgtgcac ccgaggggtt gcgaaggcgg tggactttgt acccgtcgag tctatgggaa 60
ccactatgcg gtccccggtc 80

<210> 25
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligodeoxynucleotide

<400> 25
ccacgctaag cgtaggctgg ccaggggagc acccccctcc ttggccagct c 51

<210> 26
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
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oligodeoxynucleotide

<400> 26
ccacgctaag cgtaggctgg ccaggggaga tcccccctcc ttggccagct c 51

<210> 27
<211> 3010
<212> PRT
<213> Hepatitis C virus

<400> 27

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn
1 5 10 15

Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly
20 25 30

Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala
35 40 45

Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro
50 55 60

Ile Pro Lys Ala Arg Gln Pro Glu Gly Arg Ala Trp Ala Gln Pro Gly
65 70 75 80

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Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Leu Gly Trp Ala Gly Trp
                85                  90                  95

Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro
            100                 105                 110

Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys
        115                 120                 125

Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu
    130                 135                 140

Gly Gly Ala Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp
145                 150                 155                 160

Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile
                165                 170                 175

Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Ile Pro Ala Ser Ala Tyr
            180                 185                 190

Glu Val Arg Asn Val Ser Gly Val Tyr His Val Thr Asn Asp Cys Ser
        195                 200                 205

Asn Ala Ser Ile Val Tyr Glu Ala Ala Asp Met Ile Met His Thr Pro
    210                 215                 220

Gly Cys Val Pro Cys Val Arg Glu Asn Asn Ser Ser Arg Cys Trp Val
225                 230                 235                 240

Ala Leu Thr Pro Thr Leu Ala Ala Arg Asn Ala Ser Val Pro Thr Thr
                245                 250                 255

Thr Ile Arg Arg His Val Asp Leu Leu Val Gly Ala Ala Ala Leu Cys
            260                 265                 270

Ser Ala Met Tyr Val Gly Asp Leu Cys Gly Ser Val Phe Leu Val Ala
        275                 280                 285

Gln Leu Phe Thr Phe Ser Pro Arg Arg His Glu Thr Val Gln Asp Cys
    290                 295                 300

Asn Cys Ser Ile Tyr Pro Gly His Val Thr Gly His Arg Met Ala Trp
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305                 310                 315                 320

Asp Met Met Met Asn Trp Ser Pro Thr Ala Ala Leu Val Val Ser Gln
                325                 330                 335

Leu Leu Arg Ile Pro Gln Ala Val Val Asp Met Val Ala Gly Ala His
            340                 345                 350

Trp Gly Val Leu Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp
        355                 360                 365

Ala Lys Val Leu Ile Val Met Leu Leu Phe Ala Gly Val Asp Gly Gly
    370                 375                 380

Thr Tyr Val Thr Gly Gly Thr Met Ala Lys Asn Thr Leu Gly Ile Thr
385                 390                 395                 400

Ser Leu Phe Ser Pro Gly Ser Ser Gln Lys Ile Gln Leu Val Asn Thr
                405                 410                 415

Asn Gly Ser Trp His Ile Asn Arg Thr Ala Leu Asn Cys Asn Asp Ser
            420                 425                 430

Leu Asn Thr Gly Phe Leu Ala Ala Leu Phe Tyr Val His Lys Phe Asn
        435                 440                 445

Ser Ser Gly Cys Pro Glu Arg Met Ala Ser Cys Ser Pro Ile Asp Ala
    450                 455                 460

Phe Ala Gln Gly Trp Gly Pro Ile Thr Tyr Asn Glu Ser His Ser Ser
465                 470                 475                 480

Asp Gln Arg Pro Tyr Cys Trp His Tyr Ala Pro Arg Pro Cys Gly Ile
                485                 490                 495

Val Pro Ala Ala Gln Val Cys Gly Pro Val Tyr Cys Phe Thr Pro Ser
            500                 505                 510

Pro Val Val Val Gly Thr Thr Asp Arg Phe Gly Val Pro Thr Tyr Ser
        515                 520                 525

Trp Gly Glu Asn Glu Thr Asp Val Leu Leu Leu Asn Asn Thr Arg Pro
    530                 535                 540
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Pro Gln Gly Asn Trp Phe Gly Cys Thr Trp Met Asn Ser Thr Gly Phe
545                 550                 555                 560

Thr Lys Thr Cys Gly Gly Pro Pro Cys Asn Ile Gly Gly Ile Gly Asn
                565                 570                 575

Lys Thr Leu Thr Cys Pro Thr Asp Cys Phe Arg Lys His Pro Glu Ala
            580                 585                 590

Thr Tyr Thr Lys Cys Gly Ser Gly Pro Trp Leu Thr Pro Arg Cys Leu
        595                 600                 605

Val His Tyr Pro Tyr Arg Leu Trp His Tyr Pro Cys Thr Val Asn Phe
    610                 615                 620

Thr Ile Phe Lys Val Arg Met Tyr Val Gly Gly Val Glu His Arg Leu
625                 630                 635                 640

Glu Ala Ala Cys Asn Trp Thr Arg Gly Glu Arg Cys Asn Leu Glu Asp
                645                 650                 655

Arg Asp Arg Ser Glu Leu Ser Pro Leu Leu Leu Ser Thr Thr Glu Trp
            660                 665                 670

Gln Val Leu Pro Cys Ser Phe Thr Thr Leu Pro Ala Leu Ser Thr Gly
        675                 680                 685

Leu Ile His Leu His Gln Asn Val Val Asp Val Gln Tyr Leu Tyr Gly
    690                 695                 700

Ile Gly Ser Ala Val Val Ser Phe Ala Ile Lys Trp Glu Tyr Val Leu
705                 710                 715                 720

Leu Leu Phe Leu Leu Leu Ala Asp Ala Arg Val Cys Ala Cys Leu Trp
                725                 730                 735

Met Met Leu Leu Ile Ala Gln Ala Glu Ala Ala Leu Glu Asn Leu Val
            740                 745                 750

Val Leu Asn Ala Ala Ser Val Ala Gly Ala His Gly Ile Leu Ser Phe
        755                 760                 765
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Leu Val Phe Phe Cys Ala Ala Trp Tyr Ile Lys Gly Arg Leu Val Pro
    770                 775                 780

Gly Ala Ala Tyr Ala Leu Tyr Gly Val Trp Pro Leu Leu Leu Leu Leu
785                 790                 795                 800

Leu Ala Leu Pro Pro Arg Ala Tyr Ala Met Asp Arg Glu Met Ala Ala
                805                 810                 815

Ser Cys Gly Gly Ala Val Phe Val Gly Leu Ile Leu Leu Thr Leu Ser
            820                 825                 830

Pro His Tyr Lys Leu Phe Leu Ala Arg Leu Ile Trp Trp Leu Gln Tyr
        835                 840                 845

Phe Ile Thr Arg Ala Glu Ala His Leu Gln Val Trp Ile Pro Pro Leu
    850                 855                 860

Asn Val Arg Gly Gly Arg Asp Ala Val Ile Leu Leu Thr Cys Ala Ile
865                 870                 875                 880

His Pro Glu Leu Ile Phe Thr Ile Thr Lys Ile Leu Leu Ala Ile Leu
                885                 890                 895

Gly Pro Leu Met Val Leu Gln Ala Gly Ile Thr Lys Val Pro Tyr Phe
            900                 905                 910

Val Arg Ala His Gly Leu Ile Arg Ala Cys Met Leu Val Arg Lys Val
        915                 920                 925

Ala Gly Gly His Tyr Val Gln Met Ala Leu Met Lys Leu Ala Ala Leu
    930                 935                 940

Thr Gly Thr Tyr Val Tyr Asp His Leu Thr Pro Leu Arg Asp Trp Ala
945                 950                 955                 960

His Ala Gly Leu Arg Asp Leu Ala Val Ala Val Glu Pro Val Val Phe
                965                 970                 975

Ser Asp Met Glu Thr Lys Val Ile Thr Trp Gly Ala Asp Thr Ala Ala
            980                 985                 990
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Cys Gly Asp Ile Ile Leu Gly Leu  Pro Val Ser Ala Arg  Arg Gly Arg
        995                 1000                1005


Glu Ile  His Leu Gly Pro Ala  Asp Ser Leu Glu Gly  Gln Gly Trp
    1010                1015                1020


Arg Leu  Leu Ala Pro Ile Thr  Ala Tyr Ser Gln Gln  Thr Arg Gly
    1025                1030                1035


Leu Leu  Gly Cys Ile Ile Thr  Ser Leu Thr Gly Arg  Asp Arg Asn
    1040                1045                1050


Gln Val  Glu Gly Glu Val Gln  Val Val Ser Thr Ala  Thr Gln Ser
    1055                1060                1065


Phe Leu  Ala Thr Cys Val Asn  Gly Val Cys Trp Thr  Val Tyr His
    1070                1075                1080


Gly Ala  Gly Ser Lys Thr Leu  Ala Gly Pro Lys Gly  Pro Ile Thr
    1085                1090                1095


Gln Met  Tyr Thr Asn Val Asp  Gln Asp Leu Val Gly  Trp Gln Ala
    1100                1105                1110


Pro Pro  Gly Ala Arg Ser Leu  Thr Pro Cys Thr Cys  Gly Ser Ser
    1115                1120                1125


Asp Leu  Tyr Leu Val Thr Arg  His Ala Asp Val Ile  Pro Val Arg
    1130                1135                1140


Arg Arg  Gly Asp Ser Arg Gly  Ser Leu Leu Ser Pro  Arg Pro Val
    1145                1150                1155


Ser Tyr  Leu Lys Gly Ser Ser  Gly Gly Pro Leu Leu  Cys Pro Ser
    1160                1165                1170


Gly His  Ala Val Gly Ile Phe  Arg Ala Ala Val Cys  Thr Arg Gly
    1175                1180                1185


Val Ala  Lys Ala Val Asp Phe  Val Pro Val Glu Ser  Met Glu Thr
    1190                1195
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